

# Package ‘lrgpr’

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**Title** lrgpr

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**Description** Fit a Low Rank Gaussian Process Regression (LRGPR) / Linear Mixed Model (LMM) for large datasets. These models are widely used in statistical genetics as a test of association while correcting for the confounding effects of kinship and population structure.

**Depends** R (>= 3.0.0), methods, Rcpp, RcppGSL, RcppProgress, MASS, formula.tools, BH, doParallel, bigmemory (>= 4.4.7), bigmemory.sri, aod

**LinkingTo** Rcpp, RcppGSL

**URL** <http://lrgpr.r-forge.r-project.org/>

**License** GPL (>= 2)

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AIC.lrgpr	<i>Akaike's Information Criterion (AIC)</i>
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---

**Description**

AIC for model fit by [lrgpr](#)

**Usage**

AIC.lrgpr(object, ..., k = 2)

**Arguments**

- |        |                                      |
|--------|--------------------------------------|
| object | model fit with <a href="#">lrgpr</a> |
| ...    | other arguments                      |
| k      | for compotability, not used          |

---

BIC.lrgpr	<i>Bayesian Information Criterion (BIC)</i>
-----------	---

---

**Description**

BIC for model fit by [lrgpr](#)

**Usage**

```
## S3 method for class 'lrgpr'  
BIC(object, ...)
```

**Arguments**

object	model fit with <a href="#">lrgpr</a>
...	other arguments

---

coefficients.lrgpr	<i>Extract Model Coefficients</i>
--------------------	-----------------------------------

---

**Description**

Coefficients estimated with [lrgpr](#)

**Usage**

```
## S3 method for class 'lrgpr'  
coefficients(object, ...)
```

**Arguments**

object	model fit with <a href="#">lrgpr</a>
...	other arguments

---

convertToBinary	<i>Convert ASCII to binary file</i>
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---

## Description

Converts TPED/DOSAGE/GEN files to binary format

## Usage

```
convertToBinary(filename, filenameOut, format, nthreads = detectCores(logical
= TRUE), onlyCheckFormat = FALSE, rowNames = NULL,
simpleAnnotation = TRUE)
```

## Arguments

filename	file to be converted
filenameOut	name of binary file produced
format	specify 'TPED', 'DOSAGE' or 'GEN'
nthreads	number of threads to use
onlyCheckFormat	only check the format of the input file and don't perform conversion
rowNames	Define custom rowNames
simpleAnnotation	write FILE_alleles with name, allele1, allele2. If FALSE, write chrom id genetic_position position allele1 allele2

## Details

- TPED: plink file can be in either --recode or --recode12 format
- DOSAGE: file follows plink format: <http://pngu.mgh.harvard.edu/~purcell/plink/dosage.shtml>

Example:

```
SNP A1 A2 F1 I1 F2 I2 F3 I3
rs0001 A C 0.98 0.02 1.00 0.00 0.00 0.01
rs0002 G A 0.00 1.00 0.00 0.00 0.99 0.01
```

where the F\* values correspond to the dosage values

- GEN: file follows OXFORD format

---

cooks.distance.lrgpr

*Regression Deletion Diagnostics*


---

**Description**

Basic quantities for regression deletion diagnostics from fit of `lrgpr`

**Usage**

```
## S3 method for class 'lrgpr'
cooks.distance(model, infl = lm.influence(model, do.coef =
  FALSE), res = weighted.residuals(model),
  sd = sqrt(deviance(model)/df.residual(model)), hat = infl$hat, ...)
```

**Arguments**

<code>model</code>	model fit with <code>lrgpr</code>
<code>infl</code>	influence structure as returned by <code>lm.influence</code>
<code>res</code>	residuals
<code>sd</code>	standard deviation to use
<code>hat</code>	hat values
<code>...</code>	other arguments

---

`criterion.lrgpr`      *Compute AIC/BIC/GCV for `lrgpr` model as rank changes*


---

**Description**

Evaluate information criteria to select an optimal rank for model fit by `lrgpr`

**Usage**

```
criterion.lrgpr(formula, features, order, rank = c(seq(1, 10), seq(20, 100, by
  = 10), seq(200, 1000, by = 100)))
```

**Arguments**

<code>formula</code>	standard linear modeling syntax as used in ‘lm’
<code>features</code>	matrix from which the SVD is performed
<code>order</code>	sorted indices of features. When rank is 10, <code>decomp = svd(X[,order[1:10]])</code>
<code>rank</code>	array with elements indicating the number of confounding covariates to be used in the random effect.

**See Also**

plot.criterion.lrgpr, cv.lrgpr

**Examples**

```
n = 300
p = 5000
X = matrix(sample(0:2, n*p, replace=TRUE), nrow=n)

dcmp = svd(X)

# simulate response
h_sq = .8
eta = dcmp$u[,1:2] %*% rgamma(2, 2, 1)
error_var = (1-h_sq) / h_sq * var(eta)
y = eta + rnorm(n, sd=sqrt(error_var))

# Get ordering based on marginal correlation
i = order(cor(y, X)^2, decreasing=TRUE)

# Fit AIC / BIC / GCV based on degrees of freedom
fit = criterion.lrgpr( y ~ 1, features=X, order=i)

plot(fit)
```

---

cv.lrgpr

---

*Cross-validation for lrgpr*


---

**Description**

Fit cross-validation for multiple ranks of [lrgpr](#)

**Usage**

```
cv.lrgpr(formula, features, order, nfolds = 10, rank = c(seq(0, 10), seq(20,
  100, by = 10), seq(200, 1000, by = 100)), nthreads = 1)
```

**Arguments**

formula	standard linear modeling syntax as used in ‘lm’
features	matrix from which the SVD is performed
order	sorted indices of features. When rank is 10, decomp = svd(X[,order[1:10]])
nfolds	number of training sets
rank	array with elements indicating the number of confounding covariates to be used in the random effect.
nthreads	number of threads to be used

**Examples**

```

n = 300
p = 5000
X = matrix(sample(0:2, n*p, replace=TRUE), nrow=n)

dcmp = svd(X)

# simulate response
h_sq = .8
eta = dcmp$u[,1:2] %*% rgamma(2, 2, 1)
error_var = (1-h_sq) / h_sq * var(eta)
y = eta + rnorm(n, sd=sqrt(error_var))

# Get ordering based on marginal correlation
i = order(cor(y, X)^2, decreasing=TRUE)

# Fit cross-validation
fit = cv.lrgpr( y ~ 1, features=X, order=i)

plot(fit)

```

---

df.residual.lrgpr    *Residual Degrees-of-Freedom*


---

**Description**

Residual df from fit of [lrgpr](#)

**Usage**

```
df.residual.lrgpr(object, ...)
```

**Arguments**

object	model fit with <a href="#">lrgpr</a>
...	other arguments

---

error.bar                      *Plot Error Bars*


---

**Description**

Plot error bars for a confidence interval

**Usage**

```
error.bar(x, y, upper, lower = upper, length = 0.1, ...)
```

**Arguments**

x	x-axis position
y	y-axis position
upper	height of bar above y
lower	height of bar below y
length	horizontal length of the error bar
...	arguments for arrows(...)

---

getAlleleFreq	<i>Calculate allele frequency</i>
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---

**Description**

Calculate allele frequency

**Usage**

```
getAlleleFreq(X, nthreads = detectCores(logical = TRUE), progress = TRUE)
```

**Arguments**

X	matrix where each column is a marker coded 0,1,2 or with dosage values in this range
nthreads	number of threads to use
progress	show progress bar

---

getAlleleVariance	<i>Evaluate variance for each column</i>
-------------------	--

---

**Description**

Evaluate variance for each column

**Usage**

```
getAlleleVariance(X, nthreads = detectCores(logical = TRUE),
  progress = TRUE)
```

**Arguments**

X	matrix where each column is a marker
nthreads	number of threads to use
progress	show progress bar



---

getMACHrsq	<i>Evaluate MACH <math>r^2</math> information metric for each column</i>
------------	--

---

**Description**

Evaluate MACH  $r^2$  information metric for each column

**Usage**

```
getMACHrsq(X, nthreads = detectCores(logical = TRUE), progress = TRUE)
```

**Arguments**

X	matrix where each column is a marker
nthreads	number of threads to use
progress	show progress bar

See definition in Supplementary information S3 for Marchini and Howie (2010):  
<http://www.nature.com/nrg/journal/v11/n7/extref/nrg2796-s3.pdf>.  
 #'

**References**

Marchini, J. and B. Howie. (2010) Genotype imputation for genome-wide association studies. *Nature Reviews Genetics* 11, 499-511 '

---

getMissingCount	<i>Count missing values</i>
-----------------	-----------------------------

---

**Description**

Count missing values

**Usage**

```
getMissingCount(X, nthreads = detectCores(logical = TRUE), progress = TRUE)
```

**Arguments**

X	matrix where each column is a marker
nthreads	number of threads to use
progress	show progress bar

---

glmApply	<i>Fit standard (i.e. fixed effects) linear or logistic model for many markers</i>
----------	--

---

## Description

Analogous to `lrgprApply`, but fits standard (i.e. fixed effects) linear or logistic models for many markers

## Usage

```
glmApply(formula, features, terms = NULL, family = gaussian(),
  useMean = TRUE, nthreads = detectCores(logical = TRUE), verbose = FALSE,
  progress = TRUE, cincl = c(), cexcl = c())
```

## Arguments

formula	standard linear modeling syntax as used in 'lm'. SNP is a place holder for the each successive column of features
features	a matrix where the statistical model is evaluated with SNP if formula replace by each column successively
terms	indices of the coefficients to be tested. The indices corresponding to SNP are used if terms is not specified
family	gaussian() for a continuous response, and binomial() to fit a logit model for a binary response
useMean	if TRUE, replace missing entries with column mean. Otherwise, do not evaluate the model for that column
nthreads	number of to use for parallel execution
verbose	print additional information
progress	show progress bar
cincl	column indeces of features to include for analysis
cexcl	column indeces of features to exclude for analysis

## Examples

```
# Generate data
n = 100
p = 500
X = matrix(sample(0:2, n*p, replace=TRUE), nrow=n)
y = rnorm(n)
sex = as.factor(sample(1:2, n, replace=TRUE))

# Fit model for all markers
pValues = glmApply( y ~ sex + sex:SNP, features=X, terms=c(3,4))
```

```
# Multivariate model
n = 100
p = 1000
m = 10

Y = matrix(rnorm(n*m), nrow=n, ncol=m)
X = matrix(rnorm(n*p), nrow=n, ncol=p)

res = glmApply( Y ~ SNP, features = X, terms=2)

# p-values for univariate hypothesis test of each feature against
# each response
res$pValues
```

---

glmApply2	(Experimental) faster version of glmApply
-----------	---

---

### Description

Like glmApply, by linear instead of quadratic as a function of the number of covariates. This is still experimental

### Usage

```
glmApply2(formula, features, terms = NULL, family = gaussian(),
  useMean = TRUE, nthreads = detectCores(logical = TRUE), verbose = FALSE,
  progress = TRUE, cincl = c(), cexcl = c())
```

---

influence.lrgpr	Regression Diagnostics
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---

### Description

Basic quantities for regression diagnostics from fit of `lrgpr`

### Usage

```
## S3 method for class 'lrgpr'
influence(model, ...)
```

### Arguments

model	model fit with <code>lrgpr</code>
...	other arguments

---

leverage.lrgpr	<i>Regression Diagnostics</i>
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---

**Description**

Basic quantities for regression diagnostics from fit of `lrgpr`

**Usage**

```
leverage.lrgpr(object)
```

**Arguments**

object	model fit with <code>lrgpr</code>
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---

lm.influence.lrgpr	<i>Regression Diagnostics</i>
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---

**Description**

Basic quantities for regression diagnostics from fit of `lrgpr`

**Usage**

```
lm.influence.lrgpr(object, ...)
```

**Arguments**

object	model fit with <code>lrgpr</code>
...	other arguments

---

logLik.lrgpr	<i>Extract Log-Likelihood</i>
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---

**Description**

Log-Likelihood for model fit by `lrgpr`

**Usage**

```
logLik.lrgpr(object, ...)
```

**Arguments**

object	model fit with <code>lrgpr</code>
...	other arguments

---

loss.lrgpr	<i>Loss function</i>
------------	----------------------

---

**Description**

Compare observed and fitted response under some loss function

**Usage**

```
loss.lrgpr(y, yhat, family)
```

**Arguments**

y	observed response
yhat	fitted response
family	"gaussian" or "binomial"

---

lrgpr	<i>Fit a Low Rank Gaussian Process Regression (LRGPR) / Linear Mixed Model (LMM)</i>
-------	--

---

**Description**

Fit LRGPR/LMM models that account for covariance in response values, but where the scale of the covariance is unknown. Standard linear modeling syntax is used for the model specification in addition to a covariance matrix or its eigen-decomposition.

**Usage**

```
lrgpr(formula, decomp, rank = max(ncol(decomp$u), ncol(decomp$vectors)),
      delta = NULL, nthreads = 4, W_til = NULL, scale = TRUE,
      diagnostic = FALSE)
```

**Arguments**

formula	standard linear modeling syntax as used in ‘lm’
decomp	eigen-decomposition produced from eigen(K), where K is the covariance matrix. Or singular value decomposition svd(X[,1:100]) based on a subset of markers
rank	decomposition is truncated to the first rank eigen-vectors
delta	ratio of variance components governing the fit of the model. This should be estimated from a previous evaluation of ‘lm’ on the same response and eigen-decomposition
nthreads	number of threads to use for parallel execution

W_til	markers used to construct decomp that should now be removed from construction of decomp. This is the proximal contamination term of Listgarten, et al. (2012)
scale	should W_til be scaled and centered
diagnostic	compute diagnostic statistics to be used with plot()

**Value**

coefficients	regression coefficients for each covariate
p.values	p-values from Wald test of each coefficient
sd	standard deviation of each coefficient estimate
sigSq_e	variance component $\sigma_e^2$
	corresponding to the residual error
sigSq_a	variance component $\sigma_a^2$
	corresponding the scale of the covariance, K
delta	ratio of variance components: $\sigma_e^2 / \sigma_a^2$
rank	the rank of the random effect
logLik	log-likelihood of the model fit
fitted.values	estimated response values: y_hat
alpha	BLUP of the random effect
Sigma	variance-covariate matrix of estimate of beta
hii	diagonals of the matrix H such that y_hat = Hy
y	responses
x	design matrix
df	effective degrees of freedom: trace(H) based on Hoffman (2013)
residuals	residuals of model fit: y - y_hat
AIC	Akaike information criterion
BIC	Bayesian information criterion
GCV	generalized cross-validation
eigenVectors	eigen-vectors in decomp
eigenValues	eigen-values in decomp
df.residual	n - ncol(X)
rank	rank of decomposition used, where only non-negative eigen/singular values are considered

## Details

`lrgpr` fits the model:

$$y = X\beta + \alpha + \epsilon$$

$$\alpha \sim N(0, K\sigma_a^2)$$

$$\epsilon \sim N(0, \sigma_e^2)$$

where

$$\delta = \sigma_e^2 / \sigma_a^2$$

In practice the eigen-decomposition of  $K$ , and not  $K$  itself is required. The rank can be set to use only eigen-vectors 1:rank in the model.

This package allows hypothesis tests of single coefficients using `fit$p.values` which fits a Wald test. Composite hypothesis tests of multiple coefficients are performed with `wald(fit, terms=1:3)`.

Note that likelihood ratio tests with linear mixed models do not perform well and the resulting p-values often do not follow a uniform distribution under the null (Pinheiro and Bates, 2000). We strongly advise against using it with this model.

`lrgpr` uses the algorithm of Lippert, et al. (2011).

See Hoffman (2013) for an interpretation of the linear mixed model.

## References

- Kang, H. M., et al. (2010) Variance component model to account for sample structure in genome-wide association studies. *Nature Genetics* 42, 348-54
- Lippert, C., et al. (2011) FaST linear mixed models for genome-wide association studies. *Nature Methods* 9, 525-26
- Listgarten, J., et al. (2012) Improved linear mixed models for genome-wide association studies. *Nature Methods* 8, 833-5
- Rasmussen, C. E. and Williams, C. K. I. (2006) Gaussian processes for machine learning. MIT Press
- Pinheiro, J. C. and Bates, D. M. (2000) Mixed-Effects Models in S and S-PLUS. Springer, New York
- Hoffman, G. E. (2013) Correcting for Population Structure and Kinship Using the Linear Mixed Model: Theory and Extensions. *PLoS ONE* 8(10):e75707

Note that degrees freedom and some diagnostic statistics are not currently calculated when `W_til` is specified.

## See Also

`wald`, `lrgprApply`

## Examples

```
# Generate random data
set.seed(1)
n <- 200
y <- rnorm(n)
K <- crossprod( matrix(rnorm(n*1000), ncol=n) )
age <- rpois(n, 50)
sex <- as.factor(sample(1:2, n, replace=TRUE))
decomp <- eigen(K)

# Fit the model
fit <- lrgpr( y ~ sex + age, decomp, diagnostic=TRUE)

# Print results
fit

# Print more detailed results
summary(fit)

# P-values for each covariate
fit$p.values

# Visualize fit of the model like for `lm`
par(mfrow=c(2,2))
plot(fit)

# Composite hypothesis test using Wald's test
# Joint test of coefficients 2:3
wald( fit, terms=2:3)
```

---

lrgprApply

---

*Fit a Low Rank Gaussian Process Regression (LRGPR) / Linear Mixed Model (LMM) for many markers*


---

## Description

Fit LRGPR/LMM models that account for covariance in response values, but where the scale of the covariance is unknown. It returns p-values from a Wald test equivalent to the results of using [lrgpr](#) and [wald](#), but is designed to analyze thousands of markers in a single function call.

## Usage

```
lrgprApply(formula, features, decomp, terms = NULL,
  rank = max(ncol(decomp$u), ncol(decomp$vectors)), map = NULL,
  distance = NULL, dcmp_features = NULL, W_til = NULL, scale = TRUE,
  delta = NULL, reEstimateDelta = FALSE, nthreads = detectCores(logical =
  TRUE), verbose = FALSE, progress = TRUE, cincl = c(), cexcl = c())
```



**Arguments**

formula	standard linear modeling syntax as used in 'lm'. SNP is a place holder for the each successive column of features
features	a matrix where the statistical model is evaluated with SNP if formula replace by each column successively
decomp	eigen-decomposition produced from eigen(K), where K is the covariance matrix. Or singular value decomposition svd(features[,1:100]) based on a subset of markers
terms	indices of the coefficients to be tested. The indices corresponding to SNP are used if terms is not specified
rank	decomposition is truncated to the first rank eigen-vectors
map	p x 2 matrix where each entry corresponds to a marker in features. First column is the marker names, second columns is the genetic or physical location
distance	size of the proximal contamination window in units specified by map.
dcmp_features	the indices in features of the markers used to construct dcmp
W_til	markers used to construct decomp that should now be removed from construction of decomp. This is the proximal contamination term of Listgarten, et al. (2012)
scale	should W_til be scaled and centered
delta	ratio of variance components governing the fit of the model. This should be estimated from a previous evaluation of 'lm' on the same response and eigen-decomposition
reEstimateDelta	should delta be re-estimated for every marker. Note: reEstimateDelta=TRUE is much slower
nthreads	number of to use for parallel execution
verbose	print extra information
progress	show progress bar
cincl	column indices of features to include for analysis
cexcl	column indices of features to exclude for analysis

**Examples**

```
# Generate data
n = 100
p = 500
X = matrix(sample(0:2, n*p, replace=TRUE), nrow=n)
y = rnorm(n)
sex = as.factor(sample(1:2, n, replace=TRUE))

K = tcrossprod(matrix(rnorm(n*n*3), nrow=n))
decomp = eigen(K, symmetric=TRUE)

# Fit null model
```

```
fit = lrgpr( y ~ sex, decomp)

# Fit model for all markers
pValues = lrgprApply( y ~ sex + sex:SNP, features=X, decomp, terms=c(3,4), delta=fit$delta)
```

---

```
plot.criterion.lrgpr
```

*Plot AIC/BIC/GCV values for lrgpr() model as rank changes*

---

### Description

Plots the criteria metrics returned by `criterion.lrgpr`

### Usage

```
## S3 method for class 'criterion.lrgpr'
plot(x, col = rainbow(3), ...)
```

### Arguments

<code>x</code>	list returned by <code>criterion.lrgpr</code>
<code>col</code>	array of 3 colors
<code>...</code>	other arguments

### See Also

`criterion.lrgpr`

---

```
plot.cv.lrgpr
```

*Plot Results of Cross-validation*

---

### Description

Plot results of `cv.lrgpr`, which fits cross-validation for multiple ranks of the LRGPR

### Usage

```
## S3 method for class 'cv.lrgpr'
plot(x, ylim = c(min(x$cve - x$cvse), max(x$cve + x$cvse)),
     xlim = range(x$rank), pch = 20, col = "red",
     main = "Cross validation", xlab = "# of markers used",
     ylab = "Cross validation error", ...)
```

**Arguments**

x	result of cv.lrgpr
ylim	limits of y-axis
xlim	limits of x-axis
pch	pch
col	col
main	main
xlab	xlab
ylab	ylab
...	other parameters fed to plot()

plot.lrgpr

*Plot Diagnostics for an lrgpr Object***Description**

Six plots (selectable by "which") are currently available: a plot of residuals against fitted values, a Scale-Location plot of  $\sqrt{| \text{residuals} |}$  against fitted values, a Normal Q-Q plot, a plot of Cook's distances versus row labels, a plot of residuals against leverages, and a plot of Cook's distances against leverage/(1-leverage). By default, the first three and "5" are provided.

**Usage**

```
## S3 method for class 'lrgpr'
plot(x, which = c(1L:3L, 5L),
     caption = list("Residuals vs Fitted", "Normal Q-Q", "Scale-Location",
                    "Cook's distance", "Residuals vs Leverage",
                    expression("Cook's dist vs Leverage " * h[ii]/(1 - h[ii]))), panel = if
(add.smooth) panel.smooth else points, sub.caption = NULL, main = "",
ask = prod(par("mfcol")) < length(which) && dev.interactive(), ...,
id.n = 3, labels.id = names(residuals(x)), cex.id = 0.75,
qqline = TRUE, cook.levels = c(0.5, 1),
add.smooth = getOption("add.smooth"), label.pos = c(4, 2),
cex.caption = 1)
```

**Arguments**

x	<a href="#">lrgpr</a> object.
which	if a subset of the plots is required, specify a subset of the numbers "1:6".
caption	captions to appear above the plots; "character" vector or "list" of valid graphics annotations, see "as.graphicsAnnot". Can be set to "" or "NA" to suppress all captions.
panel	panel function. The useful alternative to "points", "panel.smooth" can be chosen by "add.smooth = TRUE".

<code>sub.caption</code>	common title-above the figures if there are more than one; used as "sub" (s."title") otherwise. If "NULL", as by default, a possible abbreviated version of "deparse(x\$call)" is used.
<code>main</code>	title to each plot-in addition to "caption".
<code>ask</code>	logical; if "TRUE", the user is <code>_ask_ed</code> before each plot, see "par(ask=.)".
<code>...</code>	other parameters to be passed through to plotting functions.
<code>id.n</code>	number of points to be labelled in each plot, starting with the most extreme.
<code>labels.id</code>	vector of labels, from which the labels for extreme points will be chosen. "NULL" uses observation numbers.
<code>cex.id</code>	magnification of point labels.
<code>qqline</code>	logical indicating if a "qqline()" should be added to the normal Q-Q plot.
<code>cook.levels</code>	levels of Cook's distance at which to draw contours.
<code>add.smooth</code>	logical indicating if a smoother should be added to most plots; see also "panel" above.
<code>label.pos</code>	positioning of labels, for the left half and right half of the graph respectively, for plots 1-3.
<code>cex.caption</code>	controls the size of "caption".

**See Also**

`plot.lm`

---

<code>predict.lrgpr</code>	<i>Predict response</i>
----------------------------	-------------------------

---

**Description**

Predict response values after training with `lrgpr`. Leaving `X_test` and `K_test` as NULL returns the fitted values on the training set

**Usage**

```
predict.lrgpr(object, X_test = NULL, K_test = NULL, ...)
```

**Arguments**

<code>object</code>	model fit from <code>lrgpr</code> on training samples
<code>X_test</code>	design matrix of covariates for test samples
<code>K_test</code>	covariance matrix between samples in the test set and training set
<code>...</code>	other arguments

---

print.lrgpr	<i>Print Values</i>
-------------	---------------------

---

**Description**

Print details for fit from [lrgpr](#)

**Usage**

```
print.lrgpr(x, ...)
```

**Arguments**

x	model fit from <a href="#">lrgpr</a>
...	other arguments

---

print.summary.lrgpr	<i>Object Summaries</i>
---------------------	-------------------------

---

**Description**

Print summary for fit from [lrgpr](#)

**Usage**

```
print.summary.lrgpr(x, ...)
```

**Arguments**

x	model fit from <a href="#">lrgpr</a>
...	other arguments

---

QQ\_plot

*QQ plot*


---

### Description

QQ plot and lambda\_GC optimized for large datasets.

### Usage

```
QQ_plot(p_values, col = rainbow(min(length(p_values), ncol(p_values))),
        main = "", pch = 20, errors = TRUE, lambda = TRUE, p_thresh = 1e-06,
        showNames = FALSE, ylim = NULL, xlim = NULL, plot = TRUE,
        new = TRUE, box.lty = par("lty"), collapse = FALSE, ...)
```

### Arguments

p_values	vector, matrix or list of p-values
col	colors corresponding to the number of columns in matrix, or entries in the list
main	title
pch	pch
errors	show 95% confidence interval
lambda	calculate and show genomic control lambda. Lambda_GC is calculated using the 'median' method on p-values > p_thresh.
p_thresh	Lambda_GC is calculated using the 'median' method on p-values > p_thresh.
showNames	show column names or list keys in the legend
ylim	ylim
xlim	xlim
plot	make a plot. If FALSE, returns lambda_GC values without making plot
new	make a new plot. If FALSE, overlays QQ over current plot
box.lty	box line type
collapse	combine entries in matrix or list into a single vector
...	other arguments

### Examples

```
p = runif(1e6)
QQ_plot(p)

# get lambda_GC values without making plot
lambda = QQ_plot(p, plot=FALSE)
```

---

read.fam	<i>Read plink FAM/TFAM files</i>
----------	----------------------------------

---

**Description**

Read FAM/TFAM file into a dataframe. This function is the same as read.tfam

**Usage**

```
read.fam(file, checkFileExtension = TRUE)
```

**Arguments**

file	location of FAM/TFAM file
checkFileExtension	If TRUE, throw error if file doesn't end with fam/tfam

---

read.tfam	<i>Read plink FAM/TFAM files</i>
-----------	----------------------------------

---

**Description**

Read FAM/TFAM file into a dataframe. This function is the same as read.fam

**Usage**

```
read.tfam(file, checkFileExtension = TRUE)
```

**Arguments**

file	location of FAM/TFAM file
checkFileExtension	If TRUE, throw error if file doesn't end with fam/tfam

---

<code>residuals.lrgpr</code>	<i>Extract Model Residuals</i>
------------------------------	--------------------------------

---

**Description**

Residuals fitted with `lrgpr`

**Usage**

```
residuals.lrgpr(object, type = "working", ...)
```

**Arguments**

<code>object</code>	model fit with <code>lrgpr</code>
<code>type</code>	the type of residual, but there is only one option here
<code>...</code>	other arguments

---

<code>rstandard.lrgpr</code>	<i>Regression Deletion Diagnostics</i>
------------------------------	--

---

**Description**

Basic quantities for regression deletion diagnostics from fit of `lrgpr`

**Usage**

```
## S3 method for class 'lrgpr'  
rstandard(model, ...)
```

**Arguments**

<code>model</code>	model fit with <code>lrgpr</code>
<code>...</code>	other arguments



---

`set_missing_to_mean`*Replace Missing Values with Mean*

---

**Description**

For each column, replace NA values with the column mean

**Usage**

```
set_missing_to_mean(A)
```

**Arguments**

A	matrix
---	--------

---

`summary.lrgpr`*Summarizing LRGPR / Linear Mixed Model Fits*

---

**Description**

Print summary for fit from `lrgpr`

**Usage**

```
summary.lrgpr(object, ...)
```

**Arguments**

object	model fit from <code>lrgpr</code>
...	other arguments

---

`vcov.lrgpr`*Calculate Variance-Covariance Matrix for a `lrgpr` Object*

---

**Description**

Returns the variance-covariance matrix of the main parameters of a fitted model object

**Usage**

```
vcov.lrgpr(object, ...)
```

**Arguments**

object	model fit with <code>lrgpr</code>
...	other arguments

---

 wald

---

*Composite hypothesis test of multiple coefficients*


---

### Description

Performs a multi-dimensional Wald test against  $H_0: \beta_i \dots \beta_j = 0$  using the estimated coefficients and their variance-covariance matrix

### Usage

```
wald(fit, terms)
```

### Arguments

fit	result of fitting with <a href="#">lrgpr</a>
terms	indices of the coefficients to be tested

### Details

The Wald statistic is

$$\beta_h^T \Sigma_h^{-1} \beta_h \sim \chi_{|h|}^2$$

where

$h$

specifies the coefficients being tested and

$|h|$

is the number of entries

### See Also

[lrgpr](#)

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